

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: September 27, 2005, 20:54:04 ; Search time 125 Seconds  
(without alignments)  
11058.472 Million cell updates/sec

Title: US-10-038-854-38

Perfect score: 14495

Sequence: 1 MDVKERRPPICSLTKSRREK. .... .BLADSANNIQPLROSEIGRR 2721

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_031,\*  
1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Query Match Length DB ID

Description

!-! SIMILARITY: Contains 8 EGF-like domains.

1 14448 98.3 2715 2 09WTS6

2 12351 85.2 2346 2 09JLCl

3 11627 80.2 2590 2 09WTR4

4 10403 71.8 2765 2 09R1K2

5 10394.5 71.7 2802 2 09DR55

6 10393.5 71.7 2764 2 09WTS5

7 10189 70.3 2771 2 09WTS7

8 10001 69.0 2825 2 070465

9 9764.5 67.4 2824 2 09WTR3

10 9489 65.5 1828 2 0807D2

11 9267 63.9 1769 2 09P273

12 9035 62.3 2705 2 09W6V6

13 8972 61.9 2731 2 09WTS4

14 8884 61.3 2725 2 09UK24

15 8463.5 58.4 2144 2 09ULU2

16 8368 57.7 2192 2 0804R1

17 5447 37.6 1045 2 09NW1

18 5313 36.7 1399 2 06N022

19 5040 34.8 964 2 09W77

20 4470.5 30.8 1198 2 080TP5

21 4061.5 28.0 1086 2 09PP2P4

22 4037.5 27.9 1071 2 07ZC7

23 3930.5 27.1 2633 2 07OK12

24 3847 26.5 2731 2 061307

25 4470.5 26.5 2731 2 09VNTU

26 3839 26.5 2515 2 024551

27 3839 26.5 2731 2 018366

28 3571.5 24.6 3004 2 024550

29 3569.5 24.6 3004 2 09VYNB

30 3520.5 24.3 2754 2 07PRV4

31 3489.5 24.1 930 2 09JLCO

#### ALIGNMENTS

Score	Match	Length	DB	ID	Score	Match	Length	DB	ID	Score	Match	Length	DB	ID
32	3416	23.6	991	2	08CAT1	98.3%	991	2	08CAT1	98.3%	991	2	08CAT1	98.3%
33	3283	22.6	625	2	09ESY2	98.3%	625	2	09ESY2	98.3%	625	2	09ESY2	98.3%
34	3213.5	22.2	849	2	09NT68	98.3%	849	2	09NT68	98.3%	849	2	09NT68	98.3%
35	2809	19.4	730	2	09EM66	98.3%	730	2	09EM66	98.3%	730	2	09EM66	98.3%
36	2784	19.2	831	2	09PU49	98.3%	831	2	09PU49	98.3%	831	2	09PU49	98.3%
37	2316	16.0	442	2	09NZJ2	98.3%	442	2	09NZJ2	98.3%	442	2	09NZJ2	98.3%
38	2237	15.4	2560	2	021980	98.3%	2560	2	021980	98.3%	2560	2	021980	98.3%
39	2198.5	15.2	2531	2	08MP22	98.3%	2531	2	08MP22	98.3%	2531	2	08MP22	98.3%
40	1673.5	11.5	329	2	08BS15	98.3%	329	2	08BS15	98.3%	329	2	08BS15	98.3%
41	1533.1	10.6	337	2	09R1K0	98.3%	337	2	09R1K0	98.3%	337	2	09R1K0	98.3%
42	1178.5	8.1	272	2	09R1J9	98.3%	272	2	09R1J9	98.3%	272	2	09R1J9	98.3%
43	1155.5	8.0	266	2	09R1K1	98.3%	266	2	09R1K1	98.3%	266	2	09R1K1	98.3%
44	1154	8.0	229	2	09QZ1	98.3%	229	2	09QZ1	98.3%	229	2	09QZ1	98.3%
45	1096	7.6	536	2	Q8C8D2	98.3%	536	2	Q8C8D2	98.3%	536	2	Q8C8D2	98.3%

Q8cat1 mus musculus  
09esy2 homo sapiens  
09nt68 homo sapiens  
09em66 homo sapiens  
09pu49 gallus gallus  
09nzj2 homo sapiens  
021980 caenorhabditis  
08mp22 caenorhabditis  
08bs15 mus musculus  
09r1k0 rattus norvegicus  
09r1j9 rattus norvegicus  
09r1k1 rattus norvegicus  
09qz1 mus musculus  
Q8c8d2 mus musculus

Q8cat1 mus musculus  
09esy2 homo sapiens  
09nt68 homo sapiens  
09em66 homo sapiens  
09pu49 gallus gallus  
09nzj2 homo sapiens  
021980 caenorhabditis  
08mp22 caenorhabditis  
08bs15 mus musculus  
09r1k0 rattus norvegicus  
09r1j9 rattus norvegicus  
09r1k1 rattus norvegicus  
09qz1 mus musculus  
Q8c8d2 mus musculus

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OM protein - protein search, using sw model

Run on: September 27, 2005, 20:56:29 ; Search time 32 Seconds  
(without alignments)  
Sequence: 8181:432 Million cell updates/sec

Title: US-10-038-854-38  
Perfect score: 14495  
Sequence: 1 MDVKERRPYCSLTKSRKEK.....BLADSANNIQFLQSEIGGR 2721

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*

1: pix1:\*

2: pix2:\*

3: pix3:\*

4: pix4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. score Query length DB ID

Description

RESULT 1  
T14271  
Doc4 protein, stress-induced - mouse  
N:Alternate names: odz protein homolog  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Sep-1999 #Sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T14271  
R:Wang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zinszner, H.  
EMBO J. 17, 3619-3630, 1998  
A:Title: Identification of novel stress-induced genes downstream of chop.  
A:Reference number: Z17951; MIFD:9815054; PMID:9699432  
A:Accession: T14271  
A:Status: Preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-2825 <WAN>  
A:Cross-references: UNIPROT:O70465; EMBL:AF059485; NID:93170614; PID:93170615; PION: AAC  
C:Genetics:  
A:Gene: Doc4

Query Match Best Local Similarity 69.0% Score 10001; DB 2; length 2825; Matches 1850; Conservative 3364; Mismatches 469; Indels 180; Gaps 23;

QY 1 MDVKERRPYCSLTKSRKEK.....BLADSANNIQFLQSEIGGR 60  
Db 1 MDVKERRPYCSLTKSRKEK.....BLADSANNIQFLQSEIGGR 57

QY 61 NRVKDLVIREADEPTTROCONFTLROGLVCEPATRGLFCAENGLPHRGYSISAGSDDT 120  
Db 58 SRVKDMVQBAEBCRTGNTFLRELGIGEMTPPHGTLYRDTGLPHGYSMGASSDAD 117

QY 121 ENEAUMSREHAMILWGRGVKSGRSSCSLSSRSNSALTUTDHEM----- 164  
Db 118 EADIVLSEHPPVRLWGSSSTRSGRSCLSLSSRANSNLTDUTDHEMTECPLHCSSASSTP 177

QY 165 -----KSDSE----- 173  
Db 178 IEQSPSPPPSPANESQRRLGNGVAQPTPDSDSEBBERFVPSFLVKSSASLGVAANDHPP 237

QY 174 ASNQGOSTLQ---PLPPLSHKHOAHRH-PSITSLNRLNLTNRNQSHAP-----PA 220  
Db 238 SSLQNHPRLRTPPPLPRHTEN-ORHAAASINSLNRRNQFPRSNPSNPAFTDHSLSGPP 295

QY 221 ALPRLQQTPEASVQLOQPSWVGSNVPESR----- 250  
Db 296 AGSRQ----BPHADQDNWLNKSKIPTRNLGKOPFPGTWDQDNLIEDIFSARRDQY 350

QY 251 --HPLFVKGIGTGPFLSTATGTTMASSVTSPPPTPLPRLSRAPKPKSSKICSW 307  
Db 351 SGHFRPKG-GPSPLCCTGSPYLTSTVSPPPPLPRTFSRPAFLNPKSKCWW 409

#### ALIGNMENTS

janusin precursor,  
MSGR6 protein - rat  
transmembrane protein  
kotch protein - AF  
adhesive plaque protein  
notch4 - mouse  
gene serrate protein - f  
crumbs protein - f  
protein F1C7.4 [1]  
notch homolog - bee  
Notch homolog protein  
GPII protein precursor  
cell wall-associated  
hemopoietic protein 1  
neurogenic protein  
neurogenic repeat

Result No.	score	Query	length	DB ID
1	10001	69.0	2825	2 T14271
2	3839	26.5	2515	2 T07098
3	3534	24.4	2406	2 A54148
4	3213.5	22.2	849	2 T46253
5	2565.5	21.5	2531	2 T15743
6	1184.5	8.2	782	2 A61625
7	703	4.8	2019	1 JQ1320
8	699	4.8	201	2 A32160
9	689	4.8	184	2 T14257
10	680.5	4.7	1746	1 S119694
11	659.5	4.5	1810	2 A32230
12	637	4.4	4006	2 T09070
13	616	4.2	3566	1 A40701
14	590	4.1	4135	2 T42629
15	589	4.1	647	2 A43902
16	472.5	3.3	1620	2 T27283
17	455.5	3.1	1203	2 A49175
18	455.5	3.1	2471	2 A49128
19	448.5	3.1	3191	2 T22945
20	427.5	2.9	2703	1 A24420
21	424.5	2.9	2555	2 A40043
22	421.5	2.9	1353	1 JH0675
23	419	2.9	2531	2 S18188
24	419	2.9	2531	2 A46019
25	417.5	2.9	1064	2 A40136
26	417.5	2.9	1111	2 T26972
27	417.5	2.9	1220	2 A56136
28	417.5	2.9	2321	2 S78549
29	416.5	2.9	2318	2 S45306

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## Om protein - protein search, using sw model

Run on:

September 27, 2005, 21:02:29 ; Search time 114 Seconds  
(without alignments)  
9715.053 Million cell updates/sec

Title: US-10-038-854-38  
Perfect score: 14495  
Sequence: 1 MDVKERRPKCSLTKSRREK.....BLADSANNTIPLRQEIGRR 2721

Scoring table: BLASTM2  
Gapop 10.0 , Gapext: 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0  
Maximum DB seq length: 0

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgmn\_6/ptodata/2/pubpaa/us07\_pubcomb.pep:\*

2: /cgmn\_6/ptodata/2/pubpaa/us06\_pubcomb.pep:\*

3: /cgmn\_6/ptodata/2/pubpaa/us06\_pubcomb.pep:\*

4: /cgmn\_6/ptodata/2/pubpaa/us07\_pubcomb.pep:\*

5: /cgmn\_6/ptodata/2/pubpaa/us07\_pubcomb.pep:\*

6: /cgmn\_6/ptodata/2/pubpaa/us08\_pubcomb.pep:\*

7: /cgmn\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

8: /cgmn\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

9: /cgmn\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

10: /cgmn\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

11: /cgmn\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

12: /cgmn\_6/ptodata/2/pubpaa/us09\_pubcomb.pep:\*

13: /cgmn\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

14: /cgmn\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

15: /cgmn\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

16: /cgmn\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

17: /cgmn\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

18: /cgmn\_6/ptodata/2/pubpaa/us10\_pubcomb.pep:\*

19: /cgmn\_6/ptodata/2/pubpaa/us11\_pubcomb.pep:\*

20: /cgmn\_6/ptodata/2/pubpaa/us11\_pubcomb.pep:\*

21: /cgmn\_6/ptodata/2/pubpaa/us60\_pubcomb.pep:\*

22: /cgmn\_6/ptodata/2/pubpaa/us60\_pubcomb.pep:\*

RESULT 1  
US-10-038-854-38  
Sequence 38, Application US/10038854  
Publication No. US20040022781A1  
GENERAL INFORMATION:  
APPLICANT: SPREK, Kimberly A  
APPLICANT: Li, Li  
APPLICANT: Woien, Adam R  
APPLICANT: Vernet, Corinne  
APPLICANT: Elsen, Andrew J  
APPLICANT: Liu, Xiaohong  
APPLICANT: Malyanar, Uriel M  
APPLICANT: Shimkess, Richard A  
APPLICANT: Tchernev, Velizar  
APPLICANT: Spaderna, Steven K  
APPLICANT: Gorman, Linda  
APPLICANT: Kokuda, Ramesh  
APPLICANT: Paturajan, Meera  
APPLICANT: Gushev, Vladimir Y  
APPLICANT: Gangoli, Esha A  
APPLICANT: Guo, XiaoJia S  
APPLICANT: Shenvi, Suresh G  
APPLICANT: Rastelli, Luca  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc  
APPLICANT: Burges, Catherine B  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Elerman, Karen  
APPLICANT: Gunter, Erik  
APPLICANT: Smithson, Glenna  
APPLICANT: Milet, Isabelle  
APPLICANT: Macdougall, John R  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-230

## ALIGNMENTS

Sequence 81, Appl  
Sequence 69, Appl  
Sequence 489, Appl  
Sequence 144, Appl  
Sequence 80, Appl  
Sequence 68, Appl  
Sequence 487, Appl  
Sequence 2, Appl  
Sequence 13, Appl  
Sequence 12, Appl  
Sequence 8, Appl  
Sequence 9, Appl  
Sequence 44, Appl  
Sequence 14, Appl  
Sequence 82, Appl  
Sequence 80, Appl  
Sequence 80, Appl  
Sequence 10, Appl  
Sequence 82, Appl  
Sequence 82, Appl  
Sequence 56, Appl  
Sequence 80, Appl  
Sequence 80, Appl  
Sequence 4494, Appl  
Sequence 52, Appl  
Sequence 1687, Appl  
Sequence 928, Appl  
Sequence 4102, Appl  
Sequence 2103, Appl  
Sequence 83, Appl  
Sequence 71, Appl  
Sequence 113, Appl  
Sequence 113, Appl  
Sequence 52, Appl  
Sequence 54, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	14495	100.0	2721	15 US-10-038-854-38
2	14745	99.9	2715	15 US-10-038-854-38
3	14248	98.3	2715	15 US-10-042-865-52
4	14248	98.3	2715	15 US-10-029-020-51
5	13944.5	96.2	2628	15 US-10-038-854-40
6	13834	95.4	2613	15 US-10-038-854-42
7	12351	85.2	2346	15 US-10-072-012-491
8	11627	80.2	2040	15 US-10-072-012-490
9	10403	71.8	2765	9 US-09-808-602-84
10	10403	71.8	2765	10 US-09-808-198-72
11	10403	71.8	2765	15 US-10-072-012-488

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OM protein - protein search, using SW model

Run on: September 27, 2005, 20:57:04 ; Search time 32 Second(s)  
(without alignments)  
Sequence: 6347.503 Million cell updates/sec

Title: US-10-038-854-38  
Perfect score: 14495

Sequence: MDVKERRPYCSLTKSRREKE.....BLADSANIQFLROSEIGR 2721

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Maximum DB seq length: 0  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5b\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5b\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/5b\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/5b\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/5C0TUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
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US-08-891-845-4  
; Sequence 4, Application US/08891845  
; Patent No. 6096873

GENERAL INFORMATION:

APPLICANT: Schaefer, Gabriele M.

APPLICANT: Sliwowski, Mark

TITLE OF INVENTION: Gamma-Heregulin

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winnatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/891,845

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/021640

FILING DATE: 07/12/96

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1043

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/525-1994

TELEFAX: 415/525-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 560 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-891-845-4

Query Match

Best Local Similarity

Sequence 1, Appli

Sequence 10, Appli

Sequence 11, Appli

Sequence 12, Appli

Sequence 13, Appli

Sequence 14, Appli

Sequence 15, Appli

Sequence 16, Appli

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Sequence 199, Appli



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OM nucleic - nucleic search, using sw model

Run on:

September 26, 2005, 22:17:44 ; Search time 16507 Seconds

(without alignments)

Sequence:

1 ttggccctggggcagaatt.....actgttatttaacttaacttta 8645

19934.913 Million cell updates/sec

Scoring table:

IDENTITY\_NUC

Gapap 10.0 , Gapext 1.0

Searched:

34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:

68479088

Minimum DB seq length:

0

Maximum DB seq length:

200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gb82:\*

9: gb\_gb82:\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 is derived by analysis of the total score distribution.

### SUMMARIES

25	714.6	8.3	894	5	B0151768	BU15176 AGNCOURT
26	711.6	8.2	757	2	B0741784	BB741784 60159546
27	707.2	8.2	776	1	A0126344	A0126344 A0126844
28	700.4	8.1	916	5	B0892798	B0892798 AGNCOURT
29	698.8	8.1	818	6	CD807778	CD807778 UI-M-GHO-
30	695.6	8.0	951	5	B0839812	B0839812 AGNCOURT
31	689.4	8.0	909	4	B0980526	BP980526 602304274
32	688.4	8.0	720	7	CN391496	CN391496 170004240
33	686.4	7.9	712	7	CN391503	CN391503 170004243
34	681.8	7.9	716	7	CN391499	CN391499 17005325
35	675.8	7.8	792	2	B0898900	B0898900 601682313
36	659.4	7.6	681	2	BR382393	BR382393 601297206
37	656.4	7.6	702	4	B0670316	BM670316 UI-E-DMI-
38	655.6	7.6	854	7	CFT45232	CFT45232 UI-M-GVO-
39	652.6	7.5	834	5	B0610605	B0610605 UI-M-FCO-
40	646	7.5	658	7	CN391493	CN391493 17005321
41	645.2	7.4	770	2	B0898495	B0898495 601681396
42	642.8	7.4	819	5	CD42846	CD42846 UI-H-FHI-
43	641.4	7.4	819	5	B0443891	BO443891 UI-M-ER0-
44	640	7.4	724	4	BG419748	BG419748 672451992
45	633.4	7.3	641	7	CN391495	CN391495 170060000

### ALIGNMENTS

RESULT NO.	SCORE	QUERY LENGTH	DB ID	DESCRIPTION	REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLMED	REFERENCE	AUTHORS
1	5051.2	58.4	5094	9 AY405420	RESULT 1	AY405420	AY405420	5094 bp	DNA	linear	GSS 12-DEC-2003
2	4850	56.1	5069	9 AY405421	LOCUS	Homo sapiens	Homo sapiens	5094 bp	DNA	linear	GSS 12-DEC-2003
3	3765.8	43.6	5087	9 AY405422	DEFINITION	Homo sapiens HCM218 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.					
4	2727.2	31.5	6246	9 AY413475	ACCESSION	AY405420					
5	27.2	9.7	5970	9 AY413476	VERSION	AY405420.1	GR:39763394				
6	1455.6	16.8	2627	3 AY413477	KEYWORDS	GSS					
7	1269.6	14.7	3190	9 AY413477	SOURCE	Homo sapiens	(human)				
8	1262	14.6	2926	3 HSMW02230	ORGANISM	Bukeyo, Metzoco; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. M.D. and Cargill, M.					
9	1222.8	14.1	3038	3 AK037897	REFERENCE	1 (bases 1 to 5094)					
10	940.6	10.9	3760	3 AK031268	AUTHORS	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civekko,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Srinivas,Y.J., Adams,M.D. and Cargill,M.					
11	806.6	9.3	883	6 CDD628955	TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
12	803.4	9.3	811	1 AY119933	JOURNAL	Science 302 (5652), 1960-1963 (2003)					
13	801	9.3	826	6 CDD628950	PUBLMED	14671302					
14	796	9.2	843	1 AY124680	REFERENCE	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civekko,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Srinivas,Y.J., Adams,M.D. and Cargill,M.					
15	783.8	9.1	812	1 AY133387	AUTHORS	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tenenbaum,D.M., Civekko,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Srinivas,Y.J., Adams,M.D. and Cargill,M.					
16	780.8	9.0	809	1 AY119743	COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.					
17	776	9.0	776	6 CDD777388	FEATURES	Submitted (16-Nov-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
18	775	9.0	868	7 CKA454304	source	AK037897					
19	772.8	8.9	865	7 CK775005	ORGANISM	Homo sapiens					
20	760	8.8	848	7 CK773227	COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.					
21	747.2	8.6	795	6 CDD628956	FEATURES	AK037897					
22	738.4	8.5	798	6 CDD628958	source	AK031268					
23	727.2	8.4	861	2 BB740880	ORGANISM	Homo sapiens					
24	724.6	8.4	732	7 CN391504	COMMENT	AK037897					

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

Query Match: 58.4%; Score: 5051.2; DB: 9; Length: 5094; Best Local Similarity: 99.4%; Pred. No.: 0; Matches: 5094; Conservative: 0; Mismatches: 10; Indels: 21; Gaps: 1; Locus-tag: "HCM218"

GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 27, 2005, 05:59:11 ; Search time 3289 seconds

(Without alignments) 1574.597 Million cell updates/sec

Title: US-10-038-854-37  
 Perfect score: 8645  
 Sequence: 1 ttgggcctcgggccagatt.....actgttatttaactta 8645  
 Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 7400732 seqs, 334313751 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:  
 1: /cgm2\_6/ptodata/2/pubpna/us07\_PUBCOMB.seq:\*

2: /cgm2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgm2\_6/ptodata/2/pubpna/us07\_NEW\_PUB.seq:\*

4: /cgm2\_6/ptodata/2/pubpna/us06\_PUBCOMB.seq:\*

5: /cgm2\_6/ptodata/2/pubpna/us07\_NEW\_PUB.seq:\*

6: /cgm2\_6/ptodata/2/pubpna/us08\_NEW\_PUB.seq:\*

7: /cgm2\_6/ptodata/2/pubpna/us08\_PUBCOMB.seq:\*

8: /cgm2\_6/ptodata/2/pubpna/us09\_PUBCOMB.seq:\*

9: /cgm2\_6/ptodata/2/pubpna/us09\_PUBCOMB.seq:\*

10: /cgm2\_6/ptodata/2/pubpna/us09C\_PUBCOMB.seq:\*

11: /cgm2\_6/ptodata/2/pubpna/us09\_NEW\_PUB.seq:\*

12: /cgm2\_6/ptodata/2/pubpna/us09\_PUBCOMB.seq:\*

13: /cgm2\_6/ptodata/2/pubpna/us09\_PUBCOMB.seq:\*

14: /cgm2\_6/ptodata/2/pubpna/us09\_PUBCOMB.seq:\*

15: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

16: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

17: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

18: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

19: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

20: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

21: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

22: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

23: /cgm2\_6/ptodata/2/pubpna/us11A\_PUBCOMB.seq:\*

24: /cgm2\_6/ptodata/2/pubpna/us11\_NEW\_PUB.seq:\*

25: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

26: /cgm2\_6/ptodata/2/pubpna/us10\_PUBCOMB.seq:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### ALIGNMENTS

RESULT 1  
 US-10-038-854-37  
 ; Sequence 37, Application US/10038854  
 ; Publication No. US20040022781A1  
 GENERAL INFORMATION:  
 APPLICANT: Spitek, Kimberly A  
 Li, Li  
 APPLICANT: Wolenc, Adam R  
 APPLICANT: Vernet, Corinne  
 APPLICANT: Eisen, Andrew J  
 APPLICANT: Liu, Xiaohong  
 APPLICANT: Malyankar, Uriel M  
 APPLICANT: Shmlets, Richard A  
 APPLICANT: Tchernev, Velizar  
 APPLICANT: Spaderna, Steven K  
 APPLICANT: Gorman, Linda  
 APPLICANT: Kekuda, Ramesh  
 APPLICANT: Paturajan, Meera  
 APPLICANT: Gusev, Vladimir Y  
 APPLICANT: Gangoli, Esha A  
 APPLICANT: Guo, Xiaojia S  
 APPLICANT: Shenoy, Suresh G  
 APPLICANT: Rastelli, Luca  
 APPLICANT: Cauman, Stacie J  
 APPLICANT: Boldog, Ferenc  
 APPLICANT: Burgess, Catherine B  
 APPLICANT: Edinger, Shlomit R  
 APPLICANT: Ellerman, Karen  
 APPLICANT: Gunther, Brik  
 APPLICANT: Smithson, Glenna

Sequence 1743, AP  
 Sequence 1143, AP  
 Sequence 185, AP  
 Sequence 1, APPL  
 Sequence 79, APPL  
 Sequence 57, APPL  
 Sequence 74, APPL  
 Sequence 77, APPL  
 Sequence 62, APPL  
 Sequence 65, APPL  
 Sequence 78, APPL  
 Sequence 66, APPL  
 Sequence 43, APPL  
 Sequence 13, APPL  
 Sequence 22, APPL  
 Sequence 7, APPL  
 Sequence 81, APPL  
 Sequence 82, APPL  
 Sequence 23, APPL  
 Sequence 4101, AP  
 Sequence 427, APPL  
 Sequence 6509, APPL  
 Sequence 76, APPL  
 Sequence 64, APPL  
 Sequence 3169, AP  
 Sequence 2959, AP  
 Sequence 7176, AP  
 Sequence 38, APPL  
 Sequence 121, APPL  
 Sequence 13976, AP  
 Sequence 85, APPL  
 Sequence 75, APPL

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 22:25:30 ; Search time 892 Seconds

(without alignments) 15058.310 Million cell updates/sec

**Title:** US-10-038-854-37

**Perfect score:** 8645

**Sequence:** tttggcctcgggcagaatt.....actgttatttaactta 8645

**Scoring table:** IDENTITY\_NUC

**Gapop** 10.0 , Gapext 1.0

**Searched:** 1202784 seqs, 818138159 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

Issued\_Parents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/PC7US\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/backFiles1.seq:\*

6: /cgn2\_6/ptodata/1/ina/backFiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
C 1	709.4	8.2	2007	US-09-976-594-407
C 2	345.8	4.0	3111	US-09-891-545-1
C 3	345.8	4.0	3111	US-09-514-573-1
C 4	345.4	4.0	1680	US-09-891-845-3
C 5	345.4	4.0	1680	US-09-514-845-3
C 6	267.8	3.1	2387	US-09-891-845-11
C 7	267.8	3.1	2387	US-09-514-573-11
C 8	112.4	2.8	4	US-09-513-999C-23277
C 9	74.6	0.9	6049	US-09-793-273C-3
C 10	74.6	0.9	6049	PCT-US95-11684-3
C 11	72.2	0.8	3033	US-09-724-797-81
C 12	70	0.8	1515	US-09-902-540-8184
C 13	70	0.8	9556	US-09-902-540-982
C 14	69.6	0.8	28509	US-09-902-540-9240
C 15	68.6	0.8	6763	US-09-949-016-3399
C 16	68.6	0.8	13857	US-09-620-312D-75
C 17	68.6	0.8	34534	US-09-949-015-15141
C 18	68.4	0.8	2244	US-09-902-540-9009
C 19	68.4	0.8	12849	US-09-902-540-963
C 20	68.4	0.8	47981	US-09-797-279-1
C 21	68.2	0.8	2277	US-08-676-667-5
C 22	68.2	0.8	2277	US-08-676-974-5
C 23	68.2	0.8	2277	US-09-676-974-5
C 24	67	0.8	1260	US-09-902-540-8673
C 25	67	0.8	9191	US-09-902-540-918
C 26	66.6	0.8	4	US-08-729-273C-1
C 27	66.6	0.8	7286	PCT-US95-11684-1

**ALIGNMENTS**

RESULT 1  
US-09-976-594-407/c

Sequence 407, APP

Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: FURNESS, Michael

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976, 594

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240, 409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program

SEQ ID NO: 407

LENGTH: 2007

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6673549 474200.1

US-09-976-594-407

Query Match 8.2%; Score 709.4; DB 4; Length 2007;

Best Local Similarity 99.6%; Pred. No. 6.5e-175;

Matches 732; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Sequence 1, Appli

Sequence 2, Appli

Sequence 3, Appli

Sequence 4, Appli

Sequence 5, Appli

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

On nucleic - nucleic search, using sw model  
Run on: September 26, 2005, 18:17:29 ; Search time 277 Seconds  
(without alignments)

18766.470 Million cell updates/sec

Title: US-10-038-854-37

Perfect score: 8645

Sequence: 1 ttgggcctggggcagaatt.....actgttattaaacttta 8645

Scoring table: IDENTITY\_NUC  
Gpop 10.0 , Gapext 1.0

Searched: 43390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: GenSeq\_16Decor:/\*  
2: geneseq1980b:/\*  
3: geneseq2000b:/\*  
4: geneseq2001a:/\*  
5: geneseq2001b:/\*  
6: geneseq2002a:/\*  
7: geneseq2002b:/\*  
8: geneseq2003a:/\*  
9: geneseq2003b:/\*  
10: geneseq2003c:/\*  
11: geneseq2004a:/\*  
12: geneseq2004b:/\*  
13: geneseq2004bs:/\*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	8643.4	100.0	8645	12 ADH41968	Adh41968 Novel hum
2	8642.2	100.0	8645	6 ABQ2344	Abq2344 Human NOV
3	8615.6	99.7	8657	12 ADH41932	Adh41932 Novel hum
4	8615	99.7	8657	12 ADH41990	Adh41990 Novel hum
5	8615	99.7	8657	12 ADH41992	Adh41992 Novel hum
6	8615	99.7	8657	12 ADH41994	Adh41994 Novel hum
7	8615	99.7	8657	12 ADH41996	Adh41996 Novel hum
8	8613.8	99.6	8675	6 ABQ2343	Abq2343 Human NOV
9	8594	99.4	8636	12 ADH41998	Adh41998 Novel hum
10	8163.6	94.4	8204	12 ADH41972	Adh41972 Novel hum
11	8006.6	92.5	8473	6 ADH21673	Adh21673 Novel hum
12	7997.8	92.5	8473	6 ABQ2345	Abq2345 Human NOV
13	7895.8	91.3	8487	12 ADH41976	Adh41976 Novel hum
14	7895.8	91.3	8487	6 ABQ2346	Abq2346 Human NOV
15	6789.2	78.5	8954	12 ADH01384	Adh01384 Teneurin
16	5952.8	68.9	6810	12 ADQ2481	Adq25481 Human BOF
17	5302.9	61.4	5309	12 ADQ21673	Adq21673 Human BOF
18	3714.8	43.0	8575	6 ADH16607	Adh16607 Human NOV
19	3714.8	43.0	8575	12 ADH77271	Adh77271 Human gen
20	3614	41.8	4	4 AAH14183	Aah14183 Human cDN

#### ALIGNMENTS

21	3614	41.8	3614	13 ADR25882	Adr25882 Breast ca
22	3589.8	41.5	8438	6 ABN05378	Abn05378 Human NOV
23	3572.8	41.3	9852	12 ADH7219	Adh7219 Human gen
24	3545.6	41.0	8797	12 ADH75919	Adh75919 Marker ge
25	3502.2	40.5	8354	6 ABS2100	Ab52100 Human TEN
26	3502.2	40.5	8354	10 ADH74829	Adh74829 Murine NO
27	3482.2	40.3	9668	12 ADH71239	Adh71239 Human gen
28	3482.2	40.3	9756	12 ADH71249	Adh71249 Human gen
29	3482.2	40.3	9823	12 ADH71257	Adh71257 Human gen
30	3482.2	40.3	9825	5 AAS14085	Aas14085 Human FCT
31	3482.2	40.3	9825	12 ADH71253	Adh71253 Human gen
32	3482.2	40.3	9825	8 ACC72052	Acc72052 BCU0205B
33	3466.4	40.1	9695	10 ADB32023	Adb32023 Human FCT
34	3460.8	40.0	9826	10 ADB32028	Adb32028 Human FCT
35	3453.8	40.0	9729	5 AAS14089	Aas14089 Human FCT
36	3453.8	40.0	9729	10 ADH71251	Adh71251 Human gen
37	3453.8	40.0	9729	12 ADH71251	Adh71251 Human gen
38	3439.2	39.8	8645	6 ABT7852	Abt7852 Human cDN
39	3423.2	39.6	8574	12 ADW42261	Adw42261 Human cDN
40	3392	39.2	6999	12 ADH71273	Adh71273 Human gen
41	3270	37.8	3270	4 AAH14671	Aah14671 Human cDN
42	3264.8	37.8	9058	4 ACC72051	Acc72051 BCU0205A
43	3249.6	37.6	8355	10 ADT74841	Adt74841 Murine NO
44	3158	36.5	7781	12 ADQ9483	Adq9483 Human sof
45	3144.2	36.4	8160	12 ADH71217	Adh71217 Human gen

Adr25882 Breast ca

Abn05378 Human NOV

Adh7219 Human gen

Adh75919 Marker ge

Ab52100 Human TEN

Adh74829 Murine NO

Adh71239 Human gen

Adh71249 Human gen

Adh71257 Human gen

Adh71245 Human gen

Aas14085 Human FCT

Adh71253 Human gen

Acc72052 BCU0205B

Adb32023 Human FCT

Aas14089 Human FCT

Adb32028 Human FCT

Adh71251 Human gen

Abt7852 Human cDN

Adw42261 Human cDN

Adh71273 Human gen

Aah14671 Human cDN

Acc72051 BCU0205A

Adt74841 Murine NO

Adq9483 Human sof

Adh71217 Human gen

